FIG. 1A

```
   1  CTCTCTCAGCTTCAGAGGGAAAAAAATGGTTGTAGATTTCTGGACTTGGGAGCAGACATT   60
   1                          M  V  V  D  F  W  T  W  E  Q  T  F    12

  61  TCAAGAACTAATCCAAGAGGCAAAACCCCGGGCCACATGGACGCTGAAGTTGGATGGCAA   120
  13   Q  E  L  I  Q  E  A  K  P  R  A  T  W  T  L  K  L  D  G  N    32

 121  CCTTCAGCTAGACTGCCTGGCTCAAGGGTGGAAGCAATACCAACAGAGAGCATTTGGCTG   180
  33   L  Q  L  D  C  L  A  Q  G  W  K  Q  Y  Q  Q  R  A  F  G  W    52

 181  GTTCCGGTGTTCCTCCTGCCAGCGAAGTTGGGCTTCCGCCCAAGTGCAGATTCTGTGCCA   240
  53   F  R  C  S  S  C  Q  R  S  W  A  S  A  Q  V  Q  I  L  C  H    72

 241  CACGTACTGGGAGCACTGGACATCCCAGGGTCAGGTGCGTATGAGGCTCTTTGGCCAAAG   300
  73   T  Y  W  E  H  W  T  S  Q  G  Q  V  R  M  R  L  F  G  Q  R    92

 301  GTGCCAGAAGTGCTCCTGGTCCCAATATGAGATGCCTGAGTTCTCCTCGGATAGCACCAT   360
  93   C  Q  K  C  S  W  S  Q  Y  E  M  P  E  F  S  S  D  S  T  M   112

 361  GAGGATTCTGAGCAACCTGGTGCAGCATATACTGAAGAAATACTATGGAAATGGCACGAG   420
 113   R  I  L  S  N  L  V  Q  H  I  L  K  K  Y  Y  G  N  G  T  R   132

 421  GAAGTCTCCAGAAATGCCAGTAATCCTGGAAGTGTCCCTGGAAGGATCCCATGACACAGC   480
 133   K  S  P  E  M  P  V  I  L  E  V  S  L  E  G  S  H  D  T  A   152

 481  CAATTGTGAGGCATGCACTTTGGGCATCTGTGGACAGGGCTTAAAAAGCTGCATGACAAA   540
 153   N  C  E  A  C  T  L  G  I  C  G  Q  G  L  K  S  C  M  T  K   172

 541  GCCGTCCAAATCCCTACTCCCCCACCTAAAGACTGGGAATTCCTCACCTGGAATTGGTGC   600
 173   P  S  K  S  L  L  P  H  L  K  T  G  N  S  S  P  G  I  G  A   192

 601  TGTGTACCTCGCAAACCAAGCCAAGAACCAGTCAGCTGAGGCAAAAGAGGCTAAGGGGAG   660
 193   V  Y  L  A  N  Q  A  K  N  Q  S  A  E  A  K  E  A  K  G  S   212

 661  TGGGTATGAGAAATTAGGGCCCAGTCGAGACCCAGATCCACTGAACATCTGTGTCTTTAT   720
 213   G  Y  E  K  L  G  P  S  R  D  P  D  P  L  N  I  C  V  F  I   232

 721  TTTGCTGCTTGTATTTATTGTAGTCAAATGCTTTACATCAGAATGATGAAAATAGGCTTG   780
 233   L  L  L  V  F  I  V  V  K  C  F  T  S  E                    246

 781  CCACTTTCTCTTATTTTAATTCCATGGTAGTCAATGAACTGGCTGCCACTTTAATATAAC   840
```

FIG. 1B

```
841  TGAAAATTCATTTTGAGACCAAGCAGGATCAAGTTTGTAGAATAAACACTGGTTTCCTAG   900

901  CCATCCTCTGAAAACAGTATGAAACATGACCAAGTACATAATGGATTTAGTAATAAATAT   960

961  TGTCGAATTGCTAAAAAAAAAAAAAAAAG  989
```

FIG. 2

```
   1 ATGAGGGTTATAGAAGGGAAGGGCTTTGCCCAAGGTCTTCCTGATGTAAACTGGATCTTC   60
   1 M  R  V  I  E  G  K  G  F  A  Q  G  L  P  D  V  N  W  I  F     20

  61 AACCCAGGTTCCGGTGTTCCTCCTGCCAGCGAAGTTGGGCTTCCGCCCAAGTGCAGATTC  120
  21 N  P  G  S  G  V  P  P  A  S  E  V  G  L  P  P  K  C  R  F     40

 121 TGTGCCACACGTACTGGGAGCACTGGACATCCCAGGGTCAGGTGCCAGAAGTGCTCCTGG  180
  41 C  A  T  R  T  G  S  T  G  H  P  R  V  R  C  Q  K  C  S  W     60

 181 TCCCAATATGAGATGCCTGAGTTCTCCTCGGATAGCACCATGAGGATTCTGAGCAACCTG  240
  61 S  Q  Y  E  M  P  E  F  S  S  D  S  T  M  R  I  L  S  N  L     80

 241 GTGCAGCATATACTGAAGAAATACTATGGAAATGGCACGAGGAAGTCTCCAGAAATGCCA  300
  81 V  Q  H  I  L  K  K  Y  Y  G  N  G  T  R  K  S  P  E  M  P    100

 301 GTAATCCTGGAAGTGTCCCTGGAAGGATCCCATGACACAGCCAATTGTGAGGCATGCACT  360
 101 V  I  L  E  V  S  L  E  G  S  H  D  T  A  N  C  E  A  C  T    120

 361 TTGGGCATCTGTGGACAGGGCTTAAAAAGCTGCATGACAAAGCCGTCCAAATCCCTACTC  420
 121 L  G  I  C  G  Q  G  L  K  S  C  M  T  K  P  S  K  S  L  L    140

 421 CCCCACCTAAAGACTGGGAATTCCTCACCTGGAATTGGTGCTGTGTACCTCGCAAACCAA  480
 141 P  H  L  K  T  G  N  S  S  P  G  I  G  A  V  Y  L  A  N  Q    160

 481 GCCAAGAACCAGTCAGCTGAGGCAAAAGAGGCTAAGGGGAGTGGGTATGAGAAATTAGGG  540
 161 A  K  N  Q  S  A  E  A  K  E  A  K  G  S  G  Y  E  K  L  G    180

 541 CCCAGTCGAGACCCAGATCCACTGAACATCTGTGTCTTTATTTTGCTGCTTGTATTTATT  600
 181 P  S  R  D  P  D  P  L  N  I  C  V  F  I  L  L  L  V  F  I    200

 601 GTAGTCAAATGCTTTACATCAGAA  624
 201 V  V  K  C  F  T  S  E     208
```

FIG. 3A

```
bmy_hpp13.fas   MVVDFWTWEQ TFQELIQEAK PRATWTLKLD GNLQLDCLAQ GWKQYQQRAF
pdb1qb0.A.-     .......... .......... .......... .......... ..........

bmy_hpp13.fas   GWFRCSSCQR SWASAQVQIL CHTYWEHWTS QGQVRMRLFG QRCQKCSWSQ
pdb1qb0.A.-     .......... ...VLRSKSL CHDEIENLLD SDHRELIGDY SKAFLLQTVD

bmy_hpp13.fas   YEMPEFSSDS TMRILSNLVQ HILKKYYGNG TRKSPEMPVI LEVSLEGSHD
pdb1qb0.A.-     GKHQDL.... .KYISPETMV ALLTGKFSNI ....VDKFVI VDCRYPYEYE

bmy_hpp13.fas   TANCEACTLG ICGQGLKSCM TKPSKSLLPH LKTGNSSPGI GAVYLANQAK
pdb1qb0.A.-     GGHIKTAVNL PLERDAESFL LKS......P IAPCSLDKRV ILIFHCEFSS

bmy_hpp13.fas   NQSAEAKEAK GSGYEKLGPS RDPDPLNICV FILLLVFIVV KCFTSE....
pdb1qb0.A.-     ERGPRMCRFI RERDRAVN.. ...DYPSLYY PEMYILKGGY KEFFPQHPNF

bmy_hpp13.fas   SE........ .......... .......... .......... ..........
pdb1qb0.A.-     PQHPNFCEPQ DYRPMNHEAF KDELKTFRLK TRSWAGERSR RELCSRLQDQ
```

FIG. 3B

```
Query  -------MRVIEGKGFAQGL----PDVNWIFNPGSGVPPASEVGLPPKCRFCATRTGSTG 49
               ...|.|......|    .|.:::..|...        .|........|.|:..
Target MKSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKS--------NPGDLTLSVRRNGAVT 52

Query  HPRVRCQKCSWSQYEMPEFSSDSTMRILSNLVQHILKKYYGNGTRKSPEMPVILEVSLEG 109
       |.::::.....:..|..      .....|:.|||:.::  :....:.....:.|:..|..
Target HIKIQNTGDYYDLYGG------EKFATLAELVQYYME--HHGQLKEKNGDVIELKYPLNC 104

Query: SHDTANCEACTLGICGQGLKSCMTKPSKSLLPHLKTGNSSPGIGAVYLANQAKNQSAEAK 169
       : |..:.......:.|:..:..:|:             ....|...|..:..
Target A-DPTSERWFHGHLSGKEAEKLLTE-----------KGKHGSFLVRESQS--------- 142

Query: EAKGSGYEKLGPSRDPDPLNICVFILL-------------LVFIVVKCFTSE-------- 208
                      .|.:..:.:..              :..:::::|...:
Target ----------------HPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGER 186

Query: ---------------------------------------------------------- 208
Target FDSLTDLVEHYKKNPMVETLGTVLQLKQPLNTTRINAAEIESRVRELSKLAETTDKVKQG 246

Query: ---------------------------------------------------------- 208
Target FWEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPVSDYIN 306

Query: ---------------------------------------------------------- 208
Target ANIIMPEFETKCNNSKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSK 366

Query: ---------------------------------------------------------- 208
Target CVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDH 426

Query: ---------------------------------------------------------- 208
Target GVPSDPGGVLDFLEEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDC 486

Query: ------------------------------------ 208
Target DIDVPKTIQMVRSQRSGMVQTEAQYRSIYMAVQHYIETL 525
```

FIG. 4

```
Alignment 1 Score 492.00 (Bits)
BMSPROT:AC06831  1 MRVIEGKGFAQGLPDVNWIFNP
                    MRVIEGKGFAQGLPDVNWIFNP
                    MRVIEGKGFAQGLPDVNWIFNP
AC068318_11      1302 aagaggagtgcgccggatatac
                      tgttagagtcagtcatagttac
                      ggtaaggctcattttacgccca

BMSPROT:AC06831    23                              SGVPPASEVGLPP
                                                   SGVPPASEVGLPP
                                 G:G[ggt]          SGVPPASEVGLPP
AC068318_11      1368 GGTATGAG Intron 1    CAGGTtggccgagggccc
                       <1-----[1369 : 1970]-1>  cgtcccgatgtcc
                                                ctttccatgtgc

BMSPROT:AC06831    37 KCRFCATRTGSTGHPRV
                      KCRFCATRTGSTGHPRV
                      KCRFCATRTGSTGHPRV          R:R[agg]
AC068318_11 2012      atattgacagaagccagAGGTGCGTA Intron 2
                      aggtgccgcggcgacgt <2-----[2065 : 2090]
                      gcactcattgctatcgc

BMSPROT:AC06831    54      CQKCSWSQYEMPEFSSDSTMRILSNLVQHILKKYY
                           CQKCSWSQYEMPEFSSDSTMRILSNLVQHILKKYY
                           CQKCSWSQYEMPEFSSDSTMRILSNLVQHILKKYY
AC068318_11      2088 AAGGtcattttctgacgtttgaaaaacaacgccacaatt
                      -2> gaagcgcaaatcatccagctgttgattaattaaaa
                          cggccgcatggtgccgtccggtgccgggtaggact

BMSPROT:AC06831    90 GNGTRKSPEMPVILEVSLEGSHDTANCEACTLGICGQGL
                      GNGTRKSPEMPVILEVSLEGSHDTANCEACTLGICGQGL
                      GNGTRKSPEMPVILEVSLEGSHDTANCEACTLGICGQGL
AC068318_11      2197 gagaaatcgacgacggtcggtcgagatggtatgatgcgt
                      gagcgaccatctttatctagcaaccagacgctgtggagt
                      atcgggtaagaacgagcgaactcacttgactgcctagca

BMSPROT:AC06831   129 KSCMTKPSKSLLPHLKTGNSSPGIGAVYLANQAKNQSAE
                      KSCMTKPSKSLLPHLKTGNSSPGIGAVYLANQAKNQSAE
                      KSCMTKPSKSLLPHLKTGNSSPGIGAVYLANQAKNQSAE
AC068318_11      2314 aataaactatcccccaagattcgagggtcgacgaactgg
                      aggtcaccacttcatacgacccgtgctatcaacaaacca
                      accgaggcacacccagtgtcatatttgccacacgcgatg

BMSPROT:AC06831   168 AKEAKGSGYEKLGPSRDPDPLNICVFILLLVFIVVKCFT
                      AKEAKGSGYEKLGPSRDPDPLNICVFILLLVFIVVKCFT
                      AKEAKGSGYEKLGPSRDPDPLNICVFILLLVFIVVKCFT
AC068318_11      2431 gaggagagtgatgcacgcgccaatgtatccgtaggatta
                      caacagggaaatgcggacactatgttttttttttagtc
                      aagtggtgtgaagctacatagcctcttggtattacacta

BMSPROT:AC06831   207 SE
                      SE
                      SE
AC068318_11      2548 tg
                      ca
                      aa
```

FIG. 5

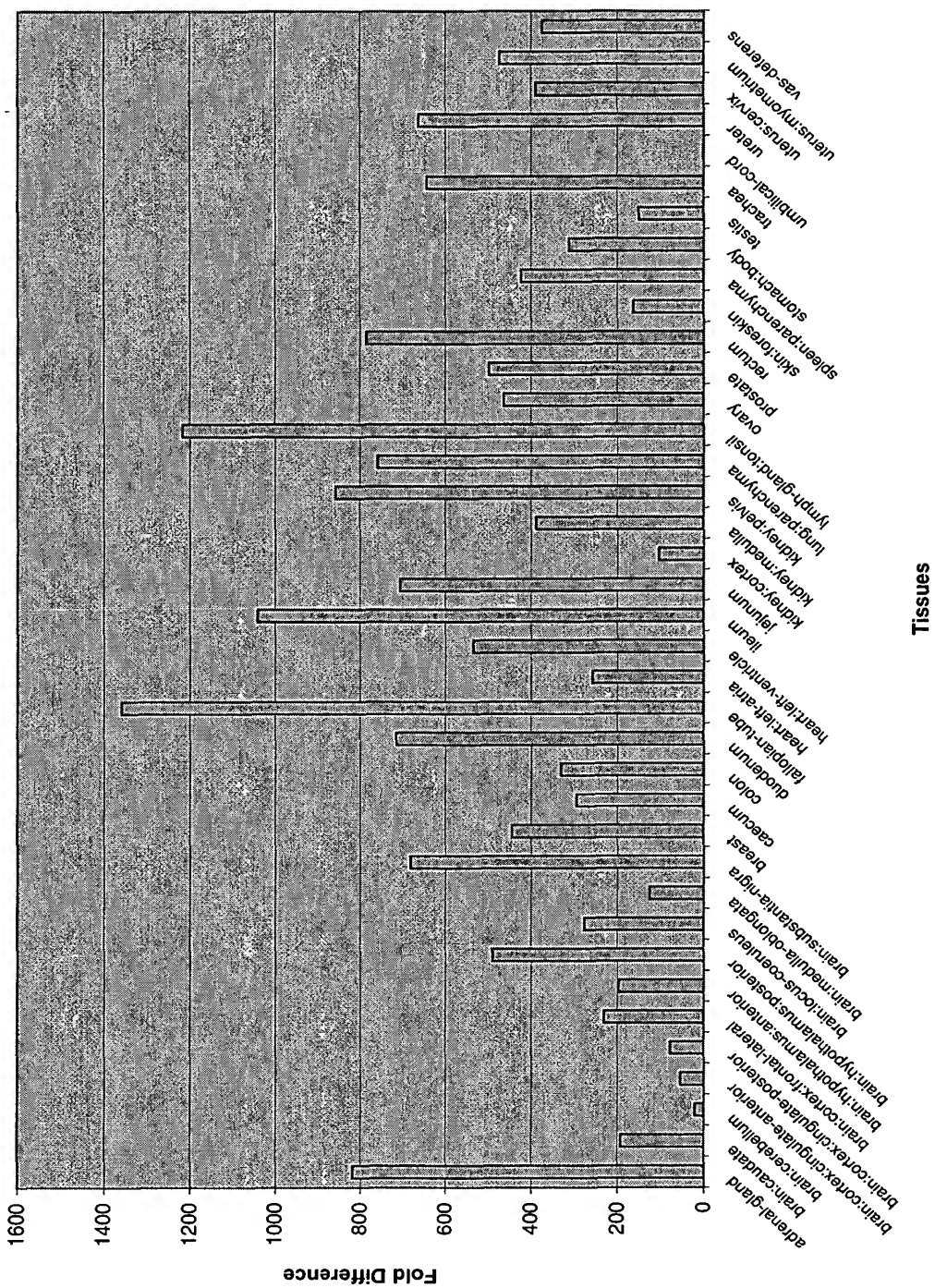
Fold Difference
1600
1400
1200
1000
800
600
400
200
0
adrenal-gland
brain:cauda
brain:cerebellum
brain:cortex:cingulate-anterior
brain:cortex:cingulate-posterior
brain:cortex:frontal-lateral
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:occus-coeruleus
brain:medulla-oblongata
brain:substantia-nigra
breast
caecum
colon
duodenum
fallopian-tube
heart:left-atria
heart:left-ventricle
ileum
jejunum
kidney:cortex
kidney:medulla
lung:parenchyma
lymph-gland:tonsil
ovary
prostate
rectum
skin:foreskin
spleen:parenchyma
stomach:body
testis
trachea
umbilical-cord
ureter
uterus:cervix
uterus:myometrium
vas-deferens
Tissues

FIG. 6

Protein	Genbank ID	Identities	Similarities
Human CDC25B protein	gi|NM_004358	18.1%	22.7%
Human Shp-2 protein	gi|4558224	30.0%	50.0%

FIG. 7

```
1aaxA       EMEKEFEQID KSGSWAAIYQ DIRHEAS... ......DFPC RVAKLPKNKN
bmy_hpp13   .......MVV DFWTWEQTFQ ELIQEAKPRA TWTLKLDGNL QL..DCLAQG

               + ++
1aaxA       RNRYRDVSPF DHSRIKLHQE DNDYINASLI KMEEAQRSYI LTQGPLPNTC
bmy_hpp13   WKQYQQRAF. .......... ........GWF RCSSCQRSWA SAQVQI..LC
               * *

1aaxA       GHFWEMVWEQ KSRGVVMLNR VMEKGSLKCA Q.YWPQKEEK EMIFEDTNLK
bmy_hpp13   HTYWEH...W TSQGQVRMRL FG....QRCQ KCSWSQYEMP EFSSDSTMRI

                                                        ++
1aaxA       LTLISEDI.K SYYTVRQLEL ENLTTQETRE ILHFHYTTWP DFGVPES...
bmy_hpp13   LSNLVQHILK KYYGNGTRKS P.....EMPV ILEVSLEGSH DTANCEACTL
                                                        *
                                                        ++++++++
1aaxA       .......... ...PASFLNF LFKVRESGSL SPEHGPVVVH SSAGIGRSGT
bmy_hpp13   GICGQGLKSC MTKPSKSLLP HLK...TGNS SPGIGAVYLA NQAKNQSAEA
                                                        ***    **

1aaxA       FCLADTCLLL MDKRKDPSSV DIKKVLLEMR KFRMGLIQTA DQLRFSYLAV
bmy_hpp13   KEAKGSGYEK LGPSRDPDPL NICVFILLLV FIVVKCFTSE ..........

1aaxA       IEGAKFIMGD SSVQDQWKEL SHED..
bmy_hpp13   .......... .......... ......
```

FIG. 8